

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/903,068C
Source: 1FW16
Date Processed by STIC: 3/21/05

ENTERED



IFW/6

RAW SEQUENCE LISTING

DATE: 03/21/2005

PATENT APPLICATION: US/09/903,068C

TIME: 14:23:24

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03192005\I903068C.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: MIYAZONO, Kohei

5 TEN DIJKE, Peter

6 FRANZEN, Petra

7 YAMASHITA, Hidetoshi

8 HELDIN, Carl-Henrik

10 (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS

11 HAVING SERINE THREONINE KINASE DOMAINS,

12 AND THEIR USE

14 (iii) NUMBER OF SEQUENCES: 48

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.

18 (B) STREET: 666 Fifth Avenue

19 (C) CITY: New York City

20 (D) STATE: New York

21 (E) COUNTRY: USA

22 (F) ZIP: 10103

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb

26 (B) COMPUTER: IBM PS/2

27 (C) OPERATING SYSTEM: PC-DOS

28 (D) SOFTWARE: Wordperfect

30 (vi) CURRENT APPLICATION DATA:

C--> 35 (A) APPLICATION NUMBER: US/09/903,068C

C--> 36 (B) FILING DATE: 11-Jul-2001

66 (vii) PRIOR APPLICATION DATA:

39 (A) APPLICATION NUMBER: PCT/GB93/02367

40 (B) FILING DATE: November 17, 1993

43 (A) APPLICATION NUMBER: GB 9224057.1

44 (B) FILING DATE: November 17, 1992

47 (A) APPLICATION NUMBER: GB 9304677.9

48 (B) FILING DATE: March 8, 1993

51 (A) APPLICATION NUMBER: GB 9304680.3

52 (B) FILING DATE: March 8, 1993

55 (A) APPLICATION NUMBER: 9311047.6

56 (B) FILING DATE: May 28, 1993

59 (A) APPLICATION NUMBER: 9313763.6

60 (B) FILING DATE: July 2, 1993

63 (A) APPLICATION NUMBER: 9316099.2

64 (B) FILING DATE: August 3, 1993

67 (A) APPLICATION NUMBER: 321344.5

68 (B) FILING DATE: October 15, 1993

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70 (viii) ATTORNEY/AGENT INFORMATION:
71 (A) NAME: Norman D. Hanson
72 (B) REGISTRATION NUMBER: 30,946
73 (C) REFERENCE/DOCKET NUMBER: LUD 5298.4 DIV (10105901)
75 (ix) TELECOMMUNICATION INFORMATION:
76 (A) TELEPHONE: (212) 318-3000
77 (B) TELEFAX: (212) 318-3400
80 (2) INFORMATION FOR SEQ ID NO: 1:
81 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 1984 base pairs
83 (B) TYPE: nucleic acid
84 (C) STRANDEDNESS: unknown
85 (D) TOPOLOGY: linear
86 (ii) MOLECULE TYPE: cDNA
87 (iii) HYPOTHETICAL: NO
C--> 88 (iv) ANTI-SENSE: NO
89 (v) FRAGMENT TYPE: internal
90 (vi) ORIGINAL SOURCE:
91 (A) ORGANISM: Homo sapiens
92 (ix) FEATURE:
93 (A) NAME/KEY: CDS
94 (B) LOCATION: 283..1791
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
96 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
97 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120
98 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180
99 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240
100 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC 294
101 Met Thr Leu Gly
102 1
103 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342
104 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
105 5 10 15 20
106 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT 390
107 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
108 25 30 35
109 GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA 438
110 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
111 40 45 50
112 GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC 486
113 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
114 55 60 65
115 TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534
116 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
117 70 75 80
118 GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582
119 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
120 85 90 95 100
121 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630

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122	Leu	Val	Leu	Glu	Ala	Thr	Gln	Pro	Pro	Ser	Glu	Gln	Pro	Gly	Thr	Asp	
123					105					110					115		
124	GGC	CAG	CTG	GCC	CTG	ATC	CTG	GGC	CCC	GTG	CTG	GCC	TTG	CTG	GCC	CTG	678
125	Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	Leu	Ala	Leu	
126					120					125					130		
127	GTG	GCC	CTG	GGT	GTC	CTG	GGC	CTG	TGG	CAT	GTC	CGA	CGG	AGG	CAG	GAG	726
128	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	
129					135					140					145		
130	AAG	CAG	CGT	GGC	CTG	CAC	AGC	GAG	CTG	GGA	GAG	TCC	AGT	CTC	ATC	CTG	774
131	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	
132					150					155					160		
133	AAA	GCA	TCT	GAG	CAG	GGC	GAC	ACG	ATG	TTG	GGG	GAC	CTC	CTG	GAC	AGT	822
134	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
135	165																
136	GAC	TGC	ACC	ACA	GGG	AGT	GGC	TCA	GGG	CTC	CCC	TTC	CTG	GTG	CAG	AGG	870
137	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	
138					185					190					195		
139	ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	GGA	AAA	GGC	CGC	918
140	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	
141					200					205					210		
142	TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG	TGG	CAC	GGT	GAG	AGT	GTG	GCC	GTC	966
143	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val	
144					215					220					225		
145	AAG	ATC	TTC	TCC	TCG	AGG	GAT	GAA	CAG	TCC	TGG	TTC	CGG	GAG	ACT	GAG	1014
146	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	Glu	Thr	Glu	
147					230					235					240		
148	ATC	TAT	AAC	ACA	GTA	TTG	CTC	AGA	CAC	GAC	AAC	ATC	CTA	GGC	TTC	ATC	1062
149	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	Gly	Phe	Ile	
150	245					250					255				260		
151	GCC	TCA	GAC	ATG	ACC	TCC	CGC	AAC	TCG	AGC	ACG	CAG	CTG	TGG	CTC	ATC	1110
152	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	
153					265					270					275		
154	ACG	CAC	TAC	CAC	GAG	CAC	GGC	TCC	CTC	TAC	GAC	TTT	CTG	CAG	AGA	CAG	1158
155	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Gln	Arg	Gln	
156					280					285					290		
157	ACG	CTG	GAG	CCC	CAT	CTG	GCT	CTG	AGG	CTA	GCT	GTG	TCC	GCG	GCA	TGC	1206
158	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	Ala	Ala	Cys	
159					295					300					305		
160	GGC	CTG	GCG	CAC	CTG	CAC	GTG	GAG	ATC	TTC	GGT	ACA	CAG	GGC	AAA	CCA	1254
161	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro	
162					310					315					320		
163	GCC	ATT	GCC	CAC	CGC	GAC	TTC	AAG	AGC	CGC	AAT	GTG	CTG	GTC	AAG	AGC	1302
164	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	Leu	Val	Lys	Ser	
165	325					330					335				340		
166	AAC	CTG	CAG	TGT	TGC	ATC	GCC	GAC	CTG	GGC	CTG	GCT	GTG	ATG	CAC	TCA	1350
167	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	His	Ser	
168					345						350				355		
169	CAG	GGC	AGC	GAT	TAC	CTG	GAC	ATC	GGC	AAC	AAC	CCG	AGA	GTG	GGC	ACC	1398
170	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	Arg	Val	Gly	Thr	

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171          360          365          370
172 AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC      1446
173 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
174          375          380          385
175 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG      1494
176 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
177          390          395          400
178 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC      1542
179 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
180 405          410          415          420
181 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG      1590
182 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
183          425          430          435
184 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT      1638
185 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
186          440          445          450
187 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG      1686
188 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
189          455          460          465
190 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG      1734
191 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
192          470          475          480
193 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA      1782
194 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
195 485          490          495          500
196 GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTC TGCC TGCAGGGGGC      1831
197 Val Ile Gln
199 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG      1891
200 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT      1951
201 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA      1984
204 (2) INFORMATION FOR SEQ ID NO: 2:
205     (i) SEQUENCE CHARACTERISTICS:
206         (A) LENGTH: 503 amino acids
207         (B) TYPE: amino acid
208         (D) TOPOLOGY: linear
209     (ii) MOLECULE TYPE: protein
210     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
211 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
212 1          5          10          15
213 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
214          20          25          30
215 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
216          35          40          45
217 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
218          50          55          60
219 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
220 65          70          75          80
221 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
222          85          90          95

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223 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
224      100      105      110
225 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
226      115      120      125
227 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
228      130      135      140
229 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
230 145      150      155      160
231 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
232      165      170      175
233 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
234      180      185      190
235 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
236      195      200      205
237 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
238      210      215      220
239 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
240 225      230      235      240
241 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
242      245      250      255
243 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
244      260      265      270
245 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
246      275      280      285
247 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
248      290      295      300
249 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
250 305      310      315      320
251 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
252      325      330      335
253 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
254      340      345      350
255 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
256      355      360      365
257 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
258      370      375      380
259 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
260 385      390      395      400
261 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
262      405      410      415
263 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
264      420      425      430
265 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
266      435      440      445
267 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
268      450      455      460
269 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
270 465      470      475      480
271 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/903,068C

DATE: 03/21/2005

TIME: 14:23:25

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03192005\I903068C.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vi)
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:88 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:284 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:493 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:712 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:912 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1112 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1306 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1511 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1709 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1903 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1916 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1929 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1942 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1955 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1981 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:2354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:2366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:2390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:2402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:2414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:2426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:2438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:2450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:2462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:2474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:2486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0